

Title : Data-Driven Reconstruction of Compartmentalized Metabolic Pathways in *Euglena gracilis* through Multi-Omics Integration

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ABSTRACT

Euglena gracilis is a highly adaptable unicellular alga with exceptional metabolic plasticity, capable of thriving under autotrophic, heterotrophic, and mixotrophic conditions. Despite its recognized biotechnological potential, its complex genome has hindered a comprehensive understanding of its metabolic pathways. In this study, we integrate transcriptomic datasets from three published studies to reconstruct key metabolic routes in *E. gracilis*. Using KEGG Orthology (KO) annotations, we map genes to metabolic functions via iPath3 and further refine these associations by converting KO numbers into Enzyme Commission (EC) identifiers.

Through Venn diagram analyses, we identify both shared and unique pathways across different trophic states, revealing distinct regulatory shifts in carbon metabolism, energy production, and secondary metabolite biosynthesis. Comparative pathway reconstruction highlights how *E. gracilis* flexibly partitions metabolic routes under varying conditions, providing new insights into its compartmentalization and metabolic adaptability.

These findings lay a crucial foundation for future metabolic modeling and the development of a genome-scale metabolic model of *E. gracilis*. Moreover, they open avenues for advanced metabolic engineering and synthetic biology applications—ranging from the sustainable production of biofuels and high-value biomolecules to novel bioprocesses—thus enhancing the organism's promise in biotechnology and green production strategies.